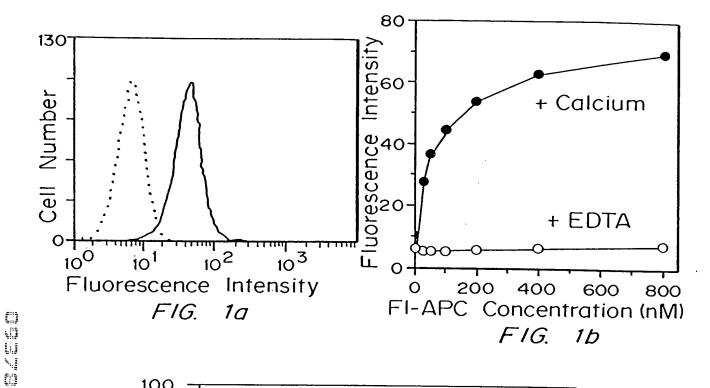
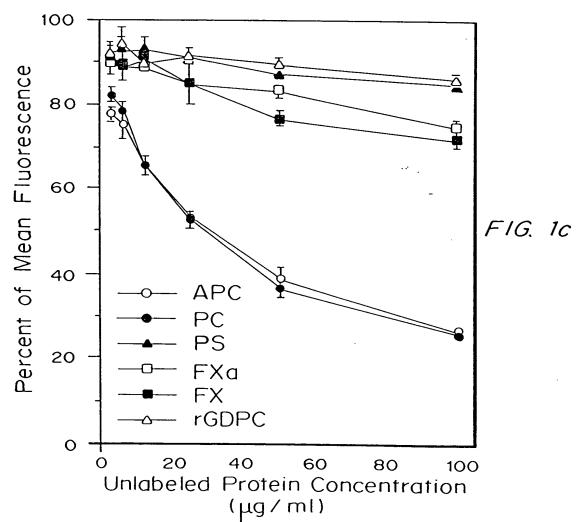


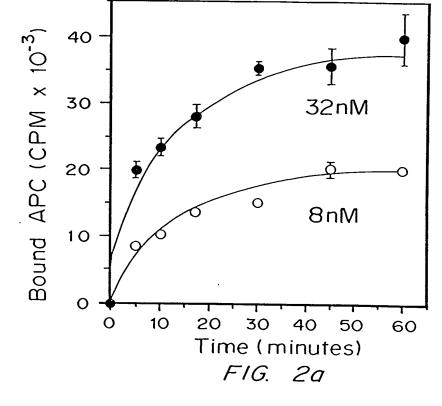
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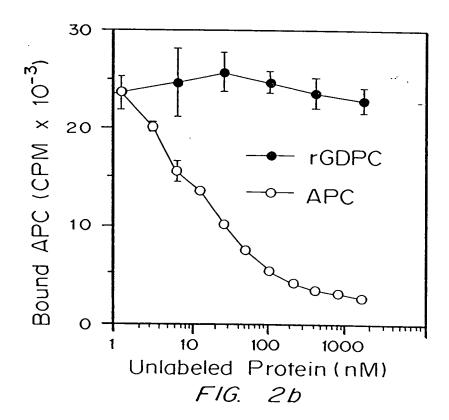




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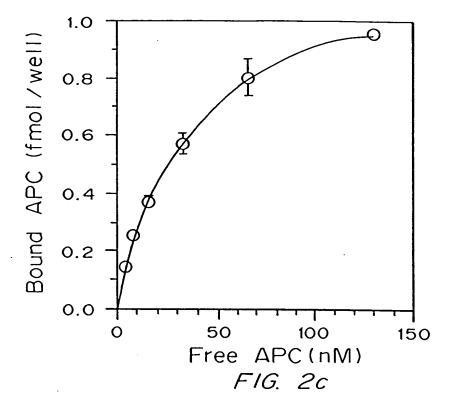
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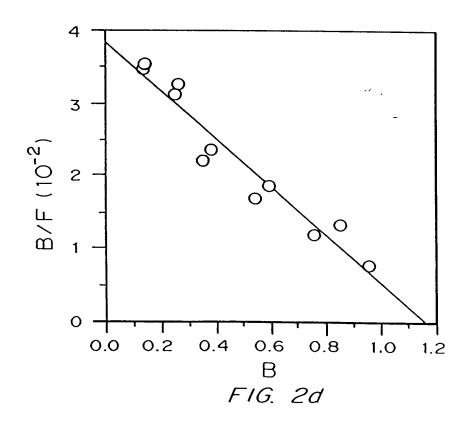


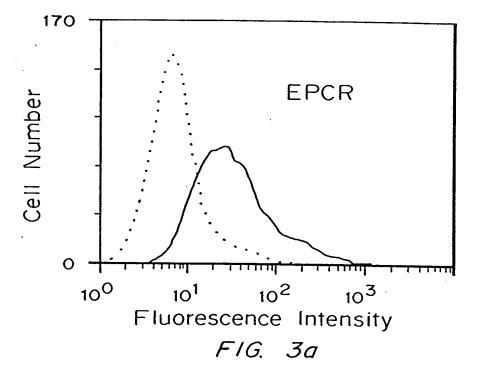


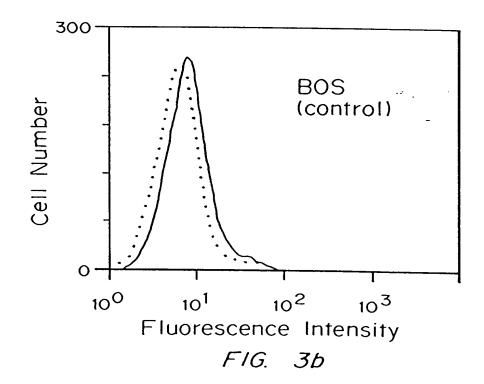
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132 CGCTGCTTCCTGGGCTGTGAGCTGCCTCCGAGGGCTCTAGAGCCCCATGTCTTCGAA ΛН V S R ල ш ۵. F L G (C) E L P (<u>C</u>)

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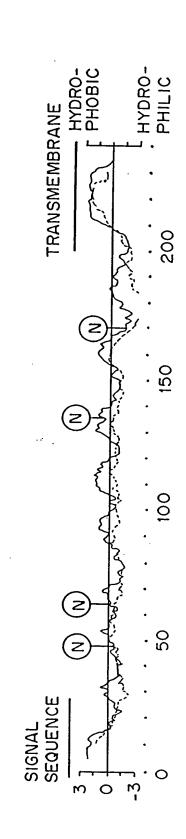
CGCACTCGGTATGAACTGCGGGAATTCCTGGAGGACACCTGTGTGCAGTATGTGCAGAAA $\overline{R}$ $\overline{T}$ $R$ $Y$ $E$ $L$ $E$ $D$ $T$ $\overline{\mathbb{C}}$ $V$ $Q$ $Y$ $V$ $Q$ $K$	009	192
GCACTCGGTATGA.  T R Y E	<b>3CAGAAA</b>	
GCACTCGGTATGA.  T R Y E	ATGT	7
GCACTCGGTATGA.  T R Y E	CAGT	Q Y
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960 1020 1140 1200 1080 GGCTGGCAAGGGAAAGTTTCAGCTCACTGTGAAGCCAGACTCCCCAACTGAAACACAGAA GGAGATGGAGAGGAGGGGGACAAGTACTTGGTTTGCTAAGAACCTAAGAACGTGTA1 GAAGTGGTGGAAATGTAAAATCCAAGTCATATGGCAGTGATCAATTATTAATCAATTAAT TCAAAAGATATAACCAAATAAACAAGTCATCCACAATCAAAATACAACATTCAATACTTC AATATTAAAAAAAAAAAAAAAAAAAAAAA 1302



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EPCR CCD41 CD1d MCD1.2

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EPCR CCD41 CD1d MCD1.2

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FYPKPVWVKWMRGEQEQQGTQPGDILPNADETWYLRATLDVVAGEAAGLSCRVKHSSLEG FYPKPVWVMWMRGDQEQQGTHRGDFLPNADETWYLQATLDVEAGEEAGLACRVKHSSLGG EPCR CCD41 CD1d MCD1.2

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......RSYTSLVLGILMGCFIIAGVAVGIFMCTSGRGLLII QDIVLYWGGSYTSMGLIALAVLACLLFLLIVGFTS.RFKRQTSYQGVL ....RSYTSLVLGVLVGGFIIAGVAVGIF EPCR CD1d CCD41

INFIVLIMLVVVVGAVVYYI.WRRRSAYQDIR QDIILYWDARQAPVGL MCD1.2

1 MLTTLLPILLLSGWAFCSQDASDGLQRLHMLQISYFRDPYHVWYQGNA48
49 SLGGHLTHVLEGPDTNTTIIQLQPLQEPESWARTQSGLQSYLLQFHGLVR 98
48 SLGKLLTHTLEGPSQNVTILQLQPWQDPESWERTESGLQIYLTQFESLVK 97
99 LVHQERTLAFPLTIRCFLGCELPPEGSRAHVFFEVAVNGSSFVSF 143
144RPERALWQADTQVTSGVVTFTLQQLNAYNRTRYELREFLEDTCVQYVQKH193   . :  .    .
194 ISAENTKGSQTSRSYTSLVLGVLVGGFIIAGVAVGIFLCTGGRRC 238

F1G. 6